

REMARKS

Claims 1-38 are pending in the application. Claim 19 has been amended without prejudice and without acquiescence. Claims 1-18, 23-33, and 36-38 have been canceled in light of the Election/Restriction requirement imposed by the Examiner as being drawn to non-elected inventions. Applicants reserve the right to pursue canceled subject matter by filing a divisional application. Applicants assert that no new matter has been added.

The issues outstanding in this application are as follows:

- The Brief Description of the Drawings has been objected to for being inconsistent with the formal drawings.
- The title of the invention has been objected to for not being descriptive of the claimed invention.
- Claims 19-22, 34, and 35 have been rejected under 35 U.S.C. § 101, in which the Office Action alleges that the claimed subject matter is directed to non-statutory algorithm type subject matter.
- Claims 19-22, 34, and 35 have been rejected under 35 U.S.C. § 102(b), in which the Office Action alleges is anticipated by Hilser *et al.*

Applicants respectfully traverse the outstanding rejections and objections, and applicants respectfully request reconsideration and withdrawal thereof in light of the remarks contained herein.

III. Issues under 35 U.S.C. § 101

Claims 19-22, 34 and 35 are rejected under 35 U.S.C. § 101 because the claimed invention is directed to non-statutory algorithm type subject matter. The Applicants respectfully disagree.

The Examiner asserts that the instant invention is non-statutory because it comprises algorithmic steps for analyzing protein data without any physical alteration resulted from said

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analysis or modeling steps. The invention comprises algorithmic steps that are limited to a practical application because independent claim 19 and its dependents comprise algorithmic steps to identify a protein fold from amino acid residues in a protein. However, in order to advance the prosecution of the present invention, Applicants have amended independent claim 19 without prejudice and without acquiescence to more specifically reflect a practical application.

In view of this amendment, Applicants respectfully request removal of this rejection.

IV. Issues under 35 U.S.C. § 102(b)

Claims 19-22, 34 and 35 are rejected under 35 U.S.C. § 102(b) as being clearly anticipated by Hilser *et al.* (1996). The Applicants respectfully disagree.

The Examiner asserts that Hilser *et al.* (1996) discloses a method of calculating the equilibrium-folding pathway of proteins as directed to different thermodynamic environments corresponding to known proteins (allegedly claim 19). However, Hilser *et al.* do not teach or suggest how to identify a protein fold. Hilser *et al.* (1996) teach probabilities of the equilibrium folding pathway. Specifically, Hilser *et al.* (1996) teach the development of a statistical description of the conformational states that become populated under equilibrium conditions (page 757, column 1, paragraph 2). The description of the probability distribution of states from the unfolded state all the way to the native state defines the equilibrium folding pathway (page 757, column 2, paragraph 3). Lastly, the probability distribution function is then used to define a series of descriptors aimed at providing a quantitative representation of the equilibrium folding pathway (page 758, column 1, paragraph 2). In order for a reference to anticipate a claim, the reference must teach every element of the claim. See *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, and *Richardson v. Suzuki Motore Co.*, 868 F.2d 1226, 1236. Since Hilser *et al.* (1996) do not teach every element of the claim, Hilser *et al.* (1996) could not have anticipated the claimed invention. Furthermore, since claims 20, 21, 22, 34 and 35 depend on claim 19, none of the claims are anticipated by Hilser *et al.* (1996).

The Examiner asserts that Hilser *et al.* (1996) present calculation of the relative heat capacity, enthalpy, and entropy of each state at the desired temperature (allegedly claim 20
25465331.1

and 22). As discussed above, Hilser *et al.* (1996) teach a statistical description of conformational states that become populated under equilibrium conditions. Even though the claimed invention may involve calculating relative heat capacity, enthalpy, and entropy, there is no way to identify protein folds because the reference does not teach or suggest how to identify protein folds.

The Examiner asserts that Figure 1 and Table 1 of Hilser *et al.* (1996) comprise scoring matrices derived of thermodynamic information for determining the distribution of amino acids (allegedly claim 21). Figure 1 is a cartoon model of the folding equilibrium for a hypothetical protein, and Table 1 is a list of conformational entropies for amino acids. Both do not comprise scoring matrices. In fact, nowhere in Hilser *et al.* (1996) is a scoring matrix taught or suggested. The instant fact pattern fail to show how Hilser *et al.* (1996) anticipate the claimed invention.

The Examiner asserts that the method of Hilser *et al.* (1996) is computer implemented (allegedly claim 34 and 35). This computer-based algorithm is aimed at estimating the entire set of statistical descriptors of the equilibrium folding pathway. For reasons stated above Hilser *et al.* (1996) do not teach or suggest all the elements of the computer-based algorithm of the claimed invention, and so the claimed invention could not have been anticipated by Hilser *et al.* (1996).

Thus, the Applicants respectfully request removal of this rejection.

V. Conclusion

Applicants assert that in view of the above remarks, each of the presently pending claims in this application is believed to be in immediate condition or allowance. Accordingly, the Examiner is respectfully requested to pass this application to issue.

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Respectfully submitted,

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1/21

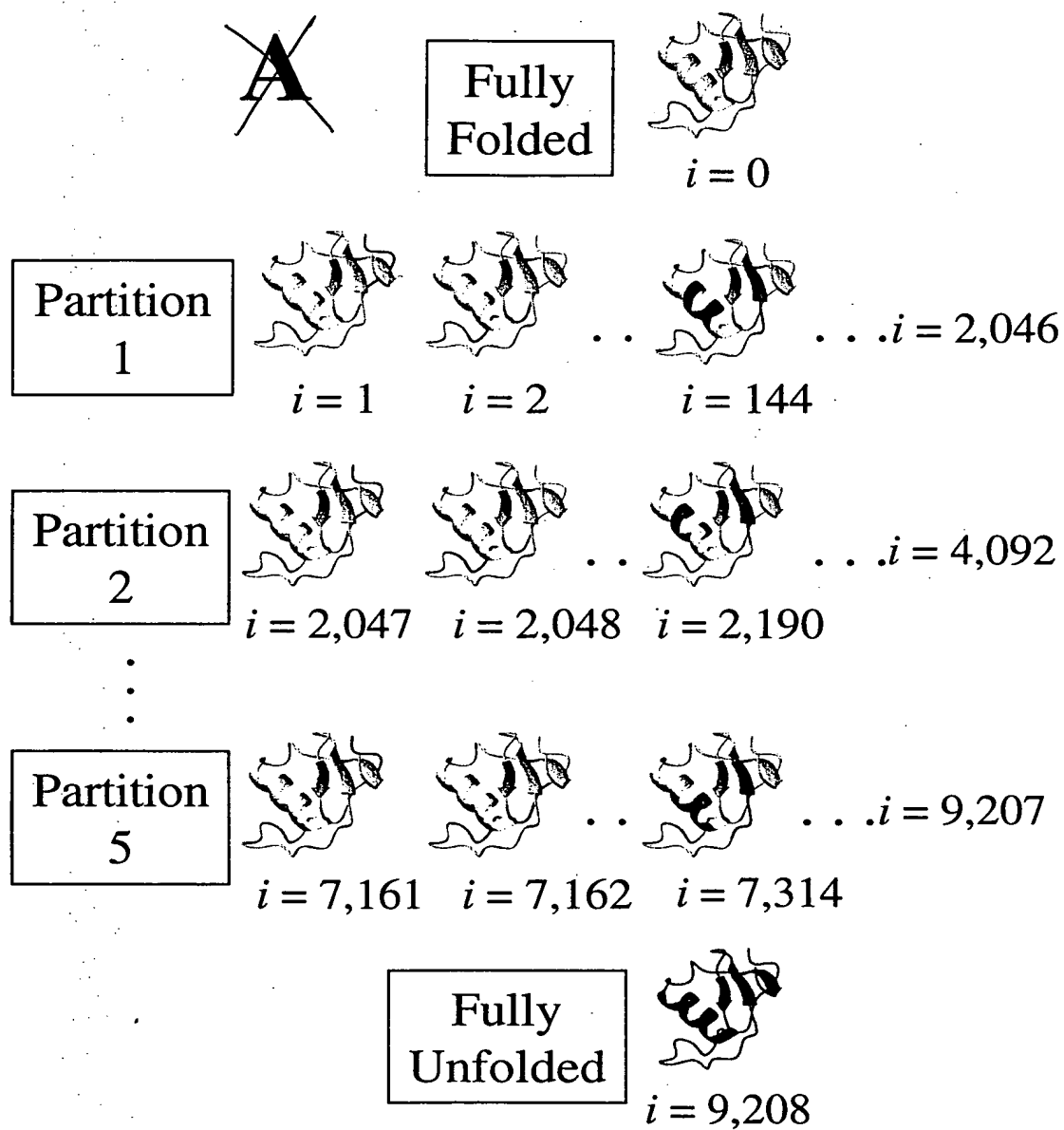


Figure 1A

2/21

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$$\Delta ASA = (ASA_{\text{unfolded unit}} + ASA_{\text{complimentary}}) - (ASA_{\text{native unit}})$$

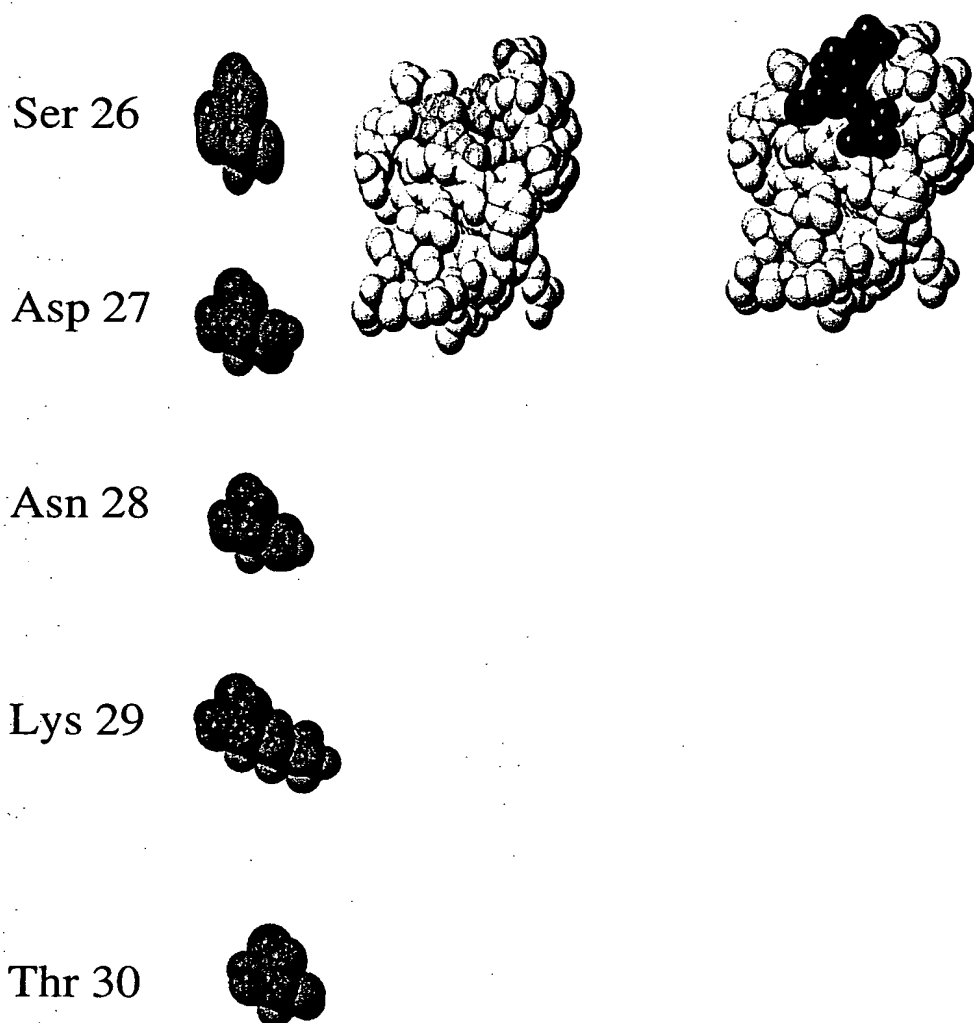


Figure 1B